

```

GCAATCGATGGGGCATCCTTTCTGAAGATCTTCGGGGCCACTGTCGTCCAGTGCCATGCAG
1  -----+-----+-----+-----+-----+ 60
CGTTAGCTACCCCGTAGGAAAGACTTCTAGAAGCCCGGTGACAGCAGGTACGGTACGTC

a   A I D G A S F L K I F G P L S S S A M Q -

TTTGTCAACGTGGGCTACTTCCTCATCGCAGCCGGCGTTGTGGTCTTTGCTCTTGGTTTC
61  -----+-----+-----+-----+-----+ 120
AAACAGTTGCACCCGATGAAGGAGTAGCGTCGGCCGCAACACCAGAAACGAGAACCAAAG

a   F V N V G Y F L I A A G V V V F A L G F -

CTGGGCTGCTATGGTGCTAAGACTGAGAGCAAGTGTGCCCTCGTGACGTTCTTCTTCATC
121 -----+-----+-----+-----+-----+ 180
GACCCGACGATACCACGATTCTGACTCTCGTTCACACGGGAGCACTGCAAGAAGAAGTAG

a   L G C Y G A K T E S K C A L V T F F F I -

CTCCTCCTCATCTTCATTGCTGAGGTTGCAGCTGCTGTGGTTCGCCTTGGTGTACACCATA
181 -----+-----+-----+-----+-----+ 240
GAGGAGGAGTAGAAGTAACGACTCCAACGTCGACGACACCAGCGGAACCACATGTGGTAT

a   L L L I F I A E V A A A V V A L V Y T I -

ATGGCTGAGCACTTCCCGACGTGCTGGTAGTGCCCTGCCATCAAGAAGATTATGGTT
241 -----+-----+-----+-----+-----+ 297
TACCGACTCGTGAAGGGCTGCAACGACCATCACGGACGGTAGTTCTTCTAATACCAA

a   M A E H F P T L L V V P A I K K I M V -

```

Fig. 1

1 AGCCAGCGAA CGGACGAGGG TGACAATAGA GTGTGGTGTC ATGCTTGTGA
51 GAGAGAAAAC ACTTTCGAGT GCCAGAACCC AAGGAGGTGC AAATGGACAG
101 AGCCATACTG CGTTATAGCG GCCGTGAAAA TATTTCACG TTTTTCATG
151 GTTGCGAACA GGTGCTCCGC TGGTTGTGCA GCGATGGAGA GACCCAAGCC
201 AGAGGAGAAG CGGTTTCTCC TGGAAGAGCC CATGCCCTTC TTTTACCTCA
251 AGTGTTGTAA A

Fig. 2